IN THE SPECIFICATION

Please replace the paragraph beginning on page 18, line 19 with the following:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(available on the worldwide web at ~~http://www.~~ddbj.nig.ac.jp/); Genebank (available on the worldwide web at the ncbi website at: ~~http:// www.ncbi.nlm.nih.gov~~/Web/Search/Index.htlm); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (~~http://www~~ available on the worldwide web at: ebi.ac.uk/ebi_docs/embl_db/embl-db.html). Other appropriate databases include dbEST (~~http://www~~ available on the worldwide web at: the ncbi website at ~~ncbi.nlm.nih.gov~~/dbEST/index.html), SwissProt (~~http://www~~ available on the worldwide web at: ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html), PIR (~~http://www~~ available on the worldwide web at: nbrt.georgetown.edu/pir/) and The Institute for Genome Research (~~http://www~~ available on the worldwide web at: tigr.org/tdb/tdb.html).

Please replace the paragraph beginning on page 20 line 18 with the following:

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance

between each pair is calculated; from this distance matrix, a guide tree is calculated and

all of the sequences are progressively aligned based on this tree. A feature of the

program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied

to encourage the insertion of gaps in probable loop regions instead of in the middle of

structured regions. Users can specify gap penalties, choose between a number of scoring

matrices, or supply their own scoring matrix for both pairwise alignments and multiple

alignments. CLUSTAL W for UNIX and VMS systems is available at the ftp site:

ebi.ac.uk. :~~ftp.ebi.ac.uk~~. Another program is MACAW (Schuler *et al.*, *Proteins Struct.*

*Func. Genet. 9:*180-190 (1991), the entirety of which is herein incorporated by reference,

for which both Macintosh and Microsoft Windows versions are available. MACAW uses

a graphical interface, provides a choice of several alignment algorithms and is available

by anonymous ftp available at the ncbi website at directory/pub/macaw. :~~

ncbi.nlm.nih.gov (directory/pub/macaw)~~.